## Figure 1

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   1  GATTCGGCACGAGAAACTTTTAAATCTTTAGTTATTTCTTAATACTTAGAACACTTAAAC   60

  61  AAAACTTTACAAAACAAAAGAGCAGAATAATTAGATCCTTTCAGGAGAATATGACTTTTT  120

 121  TTTCCTAAGCACACTGGACCATAGAGGAAGACCAAAGGAATGTACAGTTGCCTGCTCCTT  180
   1                                              M   Y   S   C   L   L   L     7

 181  CCTGACTTGCTGTATTTgACTCTGtCCCCACTGGTGGTGGCAATGCTATTAACCCCACAC  240
   8  P   D   L   L   Y   L   T   L   S   P   L   V   V   A   M   L   L   T   P   H    27

 241  TTTAACGTGGCAAATCCCCAGAATCTGTTGGCTGGTCTCTGGCTAGAGAATGAGCACAGT  300
  28  F   N   V   A   N   P   Q   N   L   L   A   G   L   W   L   E   N   E   H   S    47

 301  TTCACCCTTATGGCTCCAGAAAGAGCAAGAACACACCACTGCCAGCCAGAAGAGAGAAAA  360
  48  F   T   L   M   A   P   E   R   A   R   T   H   H   C   Q   P   E   E   R   K    67

 361  GTCTTGTTCTGTCTCTTTCCCATTGTCCCAAATAGCCAAGCACAGGTTCAACCACCCCAA  420
  68  V   L   F   C   L   F   P   I   V   P   N   S   Q   A   Q   V   Q   P   P   Q    87

 421  ATGCCACCCTTCTGCTGTGCAGCAGCCAAGGAAAAGACCCAGGAGGAGCAGCTCCAAGAA  480
  88  M   P   P   F   C   C   A   A   A   K   E   K   T   Q   E   E   Q   L   Q   E   107

 481  CCTCTGGGCAGTCAGTGCCCAGATACTTGCCCCAATTCTTTGTGTCCAAGCCACACTCAG  540
 108  P   L   G   S   Q   C   P   D   T   C   P   N   S   L   C   P   S   H   T   Q   127

 541  CTGACAAAAGCCAACACTTTGTCTCTCTTTTTTTTTTTTTCTTTTTTTTTGAGCAGAGTT  600
 128  L   T   K   A   N   T   L   S   L   F   F   F   S   F   F   L   S   R   V     147

 601  TCACTCTTGTCACCCAGGCTGGAGTGCAATGgCAGGATCTTGGCTCATTGCAACCTCCAC  660
 148  S   L   L   S   P   R   L   E   C   N   G   R   I   L   A   H   C   N   L   H   167

 661  CtCCCGGGTTCAAGCAATTCTCCTGTCTCAGCCTCTCGA   699
 168  L   P   G   S   S   N   S   P   V   S   A   S   R      180
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# Figure 2